



OIEP

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/771,208

DATE: 03/13/2002

TIME: 14:31:43

Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

3 <110> APPLICANT: MEDRANO, JUAN  
 4 BRADFORD, ERIC  
 5 HORVAT, SIMON  
 7 <120> TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE  
 9 <130> FILE REFERENCE: 407T-923710US  
 11 <140> CURRENT APPLICATION NUMBER: US 09/771,208  
 12 <141> CURRENT FILING DATE: 2001-01-26  
 14 <150> PRIOR APPLICATION NUMBER: US 08/999,477  
 15 <151> PRIOR FILING DATE: 1997-12-29  
 17 <160> NUMBER OF SEQ ID NOS: 20  
 19 <170> SOFTWARE: PatentIn version 3.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1667  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Mus musculus  
 26 <400> SEQUENCE: 1  
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 29 tagtttttagt tatttttttt tttttttttt taaacggtac gtggtcgcag acgaagaaat 120  
 31 ggaagccaga gacaagcagg tactccgctc cctgcgtctg gagctgggtg ccgagggtact 180  
 33 ggtggaagga ctggttcttc agtaccttta ccaggaagga attttgacag aaaaccacat 240  
 35 tcaagaaatc aaagctcaaa ccacaggcct ccggaagaca atgctgttgc tggacatcct 300  
 37 gccttccagg ggcctcaaaag cttttgacac cttcctcgat tccctccagg aatttccctg 360  
 39 ggtaagagag aagctggaga aggcgagaga ggaagtctca gccgagctgc ctacaggtga 420  
 41 ctggatggcc ggaatccctt cacacatcct cagcagctcg ccatcagacc agcagattaa 480  
 43 ccagctggct cagaggctag gcccgagtg ggagcccggt gtctgtcttc tgggactgtc 540  
 45 ccagaccgac atctaccgct gcaaggccaa ccatccccc aacgtgcatt cgcagggtgt 600  
 47 ggaggccttt gtccgctggc gccagcgttt tgggaagcag gccaccttc taagcttaca 660  
 49 caagggcctc caggcaatgg aggtgatcc ctccctgtc cagcacatgc tggagtgaac 720  
 51 tgaccccccc ccgcgcccc cccccacttg ctgtgggggt ggtggggcgt gggttcccaa 780  
 53 gtcacactgg ctgaaccgga cttttctcag cagggtggctt tgttctgggc ttttcagtga 840  
 55 tctgtttacg gaaagagatc gtccaccact cactcaacca tcgattggct ttaattgctt 900  
 57 gaagactgcg ctgttgtaac tatggtttgg aactttgtgg ctggccttta acaggaggcc 960  
 59 agaaaaaaca caacacccac cctacccaac cccccaaaa atcatgctac agcatcgaat 1020  
 61 gcagggtgtc tgcatacaag gcagctacac ttgtgttgcc tggagactgg attgtgcatt 1080  
 63 tagctcttga taatggtgat gataataaaa aagcaaattg tgatatagaa tgtgcctctt 1140  
 65 tcaatgagag agtattatat cacacacaca cacacacaca tacacacaca 1200  
 67 cacaccaatc ttctgttgca tagacggagg gtgtaaaaat atgggagtgg agcaagattg 1260  
 69 atagcagtca tgtgacgacg gagataaata actcaggcag gatgtataga ttaagcatga 1320  
 71 gacaccgaag ctccctgcag aggccaggga gagaacggaa gaccttcac ttaacaaatt 1380  
 73 gtatgaggag tctctgtcca ttgtttaaa gcattggatc agagacaaga gggctcagtg 1440  
 75 tttctcttga ggctgaatg gctgaaggcg gtgagttccc gaggggcgtc atgggttgct 1500  
 77 cagcctttca ttaactgcac atagtgttag ccagacaggt gtacgtgttt gtcacccat 1560  
 79 ctaagagact gaagcaggag gatcacctgt acatgactgc ttctttcaac attttaaaat 1620

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81 gtgtaacttc tattaaattc tctcagtgca aaaaaaaaaa aaaaaaa 1667
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 304
86 <212> TYPE: DNA
87 <213> ORGANISM: Mus musculus
89 <400> SEQUENCE: 2
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92 gaggtactgg tggaaggact ggttcttcag tacctttacc aggaaggaat ttgacagaa 120
94 aaccacattc aacaaatcaa agctcaaacc acaggcctcc ggaagacaat gctgttgctg 180
96 gacatcctgc cttccagggg ccccaaagct ttgacacct tcctcgattc cctccaggaa 240
98 tttccctggg taagagagaa gctggagaag gcgagagagg aagtctcagc cgagctgcct 300
100 acag 304
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104 <211> LENGTH: 160
105 <212> TYPE: DNA
106 <213> ORGANISM: bovine sp
108 <400> SEQUENCE: 3
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111 ggtactggtg gaggggctag tcctccagta tctttatcag gaaggggtct tgacagaaa 120
113 ccacgttcaa gaaattaaag ctcaagccac aggcctccg 160
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 539
118 <212> TYPE: PRT
119 <213> ORGANISM: Mus musculus
121 <400> SEQUENCE: 4
123 Met Glu Thr Gly Leu Ala Leu Ala Ala Arg Gly Ala Ser Pro Leu Tyr
124 1 5 10 15
126 Ser Gly Leu Asn Val Ala Leu Leu Glu Ala Arg Gly Ser Glu Arg Leu
127 20 25 30
129 Glu Ala Arg Gly Leu Glu Gly Leu Leu Glu Gly Leu Tyr Ala Leu Ala
130 35 40 45
132 Gly Leu Val Ala Leu Leu Glu Val Ala Leu Gly Leu Gly Leu Tyr Leu
133 50 55 60
135 Glu Val Ala Leu Leu Glu Gly Leu Asn Thr Tyr Arg Leu Glu Thr Tyr
136 65 70 75 80
138 Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile Leu Glu Leu Glu Thr His
139 85 90 95
141 Arg Gly Leu Ala Ser Asn His Ile Ser Ile Leu Glu Gly Leu Asn Gly
142 100 105 110
144 Leu Ile Leu Glu Leu Tyr Ser Ala Leu Ala Gly Leu Asn Thr His Arg
145 115 120 125
147 Thr His Arg Gly Leu Tyr Leu Glu Ala Arg Gly Leu Tyr Ser Thr His
148 130 135 140
150 Arg Met Glu Thr Leu Glu Leu Glu Leu Glu Ala Ser Pro Ile Leu Glu
151 145 150 155 160
153 Leu Glu Pro Arg Ser Glu Arg Ala Arg Gly Gly Leu Tyr Pro Arg Leu
154 165 170 175
156 Tyr Ser Ala Leu Ala Pro His Glu Ala Ser Pro Thr His Arg Pro His
157 180 185 190

```

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Input Set : A:\407T-923710US.txt

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159 Glu Leu Glu Ala Ser Pro Ser Glu Arg Leu Glu Gly Leu Asn Gly Leu  
 160 195 200 205  
 162 Pro His Glu Pro Arg Thr Arg Pro Val Ala Leu Ala Arg Gly Gly Leu  
 163 210 215 220  
 165 Leu Tyr Ser Leu Glu Gly Leu Leu Tyr Ser Ala Leu Ala Ala Arg Gly  
 166 225 230 235 240  
 168 Gly Leu Gly Leu Val Ala Leu Ser Glu Arg Ala Leu Ala Gly Leu Leu  
 169 245 250 255  
 171 Glu Pro Arg Thr His Arg Gly Leu Tyr Ala Ser Pro Thr Arg Pro Met  
 172 260 265 270  
 174 Glu Thr Ala Leu Ala Gly Leu Tyr Ile Leu Glu Pro Arg Ser Glu Arg  
 175 275 280 285  
 177 His Ile Ser Ile Leu Glu Leu Glu Ser Glu Arg Ser Glu Arg Ser Glu  
 178 290 295 300  
 180 Arg Pro Arg Ser Glu Arg Ala Ser Pro Gly Leu Asn Gly Leu Asn Ile  
 181 305 310 315 320  
 183 Leu Glu Ala Ser Asn Gly Leu Asn Leu Glu Ala Leu Ala Gly Leu Asn  
 184 325 330 335  
 186 Ala Arg Gly Leu Glu Gly Leu Tyr Pro Arg Gly Leu Thr Arg Pro Gly  
 187 340 345 350  
 189 Leu Pro Arg Val Ala Leu Val Ala Leu Leu Glu Ser Glu Arg Leu Glu  
 190 355 360 365  
 192 Gly Leu Tyr Leu Glu Ser Glu Arg Gly Leu Asn Thr His Arg Ala Ser  
 193 370 375 380  
 195 Pro Ile Leu Glu Thr Tyr Arg Ala Arg Gly Cys Tyr Ser Leu Tyr Ser  
 196 385 390 395 400  
 198 Ala Leu Ala Ala Ser Asn His Ile Ser Pro Arg His Ile Ser Ala Ser  
 199 405 410 415  
 201 Asn Val Ala Leu His Ile Ser Ser Glu Arg Gly Leu Asn Val Ala Leu  
 202 420 425 430  
 204 Val Ala Leu Gly Leu Ala Leu Ala Pro His Glu Val Ala Leu Ala Arg  
 205 435 440 445  
 207 Gly Thr Arg Pro Ala Arg Gly Gly Leu Asn Ala Arg Gly Pro His Glu  
 208 450 455 460  
 210 Gly Leu Tyr Leu Tyr Ser Gly Leu Asn Ala Leu Ala Thr His Arg Pro  
 211 465 470 475 480  
 213 His Glu Leu Glu Ser Glu Arg Leu Glu His Ile Ser Leu Tyr Ser Gly  
 214 485 490 495  
 216 Leu Tyr Leu Glu Gly Leu Asn Ala Leu Ala Met Glu Thr Gly Leu Ala  
 217 500 505 510  
 219 Leu Ala Ala Ser Pro Pro Arg Ser Glu Arg Leu Glu Leu Glu Gly Leu  
 220 515 520 525  
 222 Asn His Ile Ser Met Glu Thr Leu Glu Gly Leu  
 223 530 535  
 225 <210> SEQ ID NO: 5  
 226 <211> LENGTH: 20  
 227 <212> TYPE: DNA  
 C--> 228 <213> ORGANISM: Artificial  
 230 <220> FEATURE:

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Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

231 <223> OTHER INFORMATION: PCR primer  
 233 <400> SEQUENCE: 5  
 234 tggaagccag agacaagcag 20  
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C--> 240 <213> ORGANISM: Artificial  
 242 <220> FEATURE:  
 243 <223> OTHER INFORMATION: PCR primer  
 245 <400> SEQUENCE: 6  
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 254 <220> FEATURE:  
 255 <223> OTHER INFORMATION: PCR primer  
 257 <400> SEQUENCE: 7  
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 261 <210> SEQ ID NO: 8  
 262 <211> LENGTH: 21  
 263 <212> TYPE: DNA

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 266 <220> FEATURE:  
 267 <223> OTHER INFORMATION: PCR primer  
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 274 <211> LENGTH: 13908  
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 278 <400> SEQUENCE: 9  
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 281 aaaacacatg ctatgggttg aatggaaaaa tatcccatga aggcttatgt atttgagtca 120  
 283 cttcttagct ggtagcactc acttttgaag gctgtaaagc cttcaatctg tgggtcctac 180  
 285 ccctttggca aaccttgatc tccaaagtta cataagcaca ggcacacact tccacttcct 240  
 287 ctgaggtttt ctaccaagaa aggatcaacc attcataaaa tgttggtcct agtgaaccct 300  
 289 gcacattgta gaggcttaaa aagtttaatt tgggcctcca actcactaca caggaactcc 360  
 291 agcgggatcc gcctgtccgt tcatgctaac ctttcaccga catcttggtt ttaagtttac 420  
 293 agaaaacggt agggaccta agaaggtcat tacattacag tacattacag tacaacagaa 480  
 295 gttacaaagt agcaatgagg ggcttgagg tttagctcag tgctagagcg cttgcctagc 540  
 297 aagtgcgaag ccttaggttc ggtcctcagc tctgaaaaat caaaacaaa caaaacaaa 600  
 299 tagcaatgat aataatttta tggttgagg gtcaccatga tatgagggaac tgtattaaac 660  
 301 ggtcgtgca ttagggagga tgaggaccac tgtggggctc agctgaagga agtgagttgc 720  
 303 tgggtgtagg caccggagtg ctatgatgaa accgggttcc tgtctccctt ctaaggctga 780  
 305 ctgcaccact aattcctgcc tcccgtggag ggtgctttcc aggtcccaag ccttctgcc 840  
 307 atgttggaat gtgtcctgtg aaccatgaac cgagatcaat ctttctccc tccatcacc 900  
 309 tctgccaggt ggtttggtca tagtactcag tagagtaagg aggtcggaag atttactaca 960  
 311 cctgacaaa gaaaaatta ctgtatgatc tcaaaaaaaa aaaaaaaaaa aacaccacca 1020

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313 ccaacaacaa aaaaaccaac aaaaaaccaa aaccctttag gagtgcagaa gcacaggcac 1080  
315 acacttccac ttctcttgag gttttctacc aagaaaggat caaccattca taaaacgttg 1140  
317 gtcttagtta tccctgcaca ttgtagaggc ttaaaaagtt taacttgggc ctccaactca 1200  
319 ctacacagaa ctccagaggg atccgcctgt ccgttcatgc taacctttca ccgacatctt 1260  
321 gtttttaagt ttacagaaaa cgttagggac ctaaagaagg taagcatcct gctaagttac 1320  
323 tccctggctt tacacaggct ttctaaaact tgagtaagag gcacccctcc catcaaagat 1380  
325 tccaggaaaa cagcctcccc cctccgcggc cacacatacg aatctatcgc tgacaaagcc 1440  
327 cctgtaagct ggcttatgtc ctccctcgc gttcaccatt ctgtaagtgc atagaattat 1500  
329 ttaagaggaa aaaaattact gtggataaaa attggttcgg gcccttggaa ttggccggtc 1560  
331 gtgttggtt tccctccagg gccgcaggc ggggcaccag gcaaggcttg gaagccgcgc 1620  
333 ctctctcaac ctctcctggc cacccttgcc caacttcccc atagacacag cttcaactaa 1680  
335 aagtggccat tgacctttca agcttttgag cagtggggca acagaacagt atttcaaaga 1740  
337 aaaatggtta tcgaaatttc gaatccgggt ttcccatgag tgtttttttt ttgttttggt 1800  
339 tttctgttaa aaaaaaaaaa agtaggtcac attcaaagtg ggtcacgttt caggagccgg 1860  
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343 caataggaaa gaagtactgg gatcaatacg aactccgggt ccctggcttt gcaaggattc 1980  
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367 accagacca gcacccgcac cggctctctc caccggctc ccttgaagcc tgcgcattag 2700  
369 cggccggggc ctctttaaag cgttgccggg ggtgcggtc acgtgaggcg gattcctgga 2760  
371 aagttcctgg aaagcggcct ccgcgcggc cgggcggggc gcgagggcg ggaggcggg 2820  
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375 ttaactcttg ccaagctctc ccgcctctgc ggtcccggg ccttgggctt cccccctgaa 2940  
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387 tgggtctcgg gaaattttcc gagcaccccc acccccacac aactgctacc caaatttata 3300  
389 atcctaataa cctgatctcc cgtcctccc cgcagcctc cgccttgcct ccccccccc 3360  
391 acccttctc tttctcccat ctctccgct tcaactggag ggaaaccogg cactggcgag 3420  
393 cagggtgtgc agcctggggc ggagaggggg gggggaagct aggcagcgat cctgggatt 3480  
395 tttgtctgcc tttggcgca aaaaactcgg ttgcttttac tgagcgagga gccgattgca 3540  
397 tccccagcca tctccttcca caaataaacg tcaaccgggg aactcagacg gacacccctc 3600  
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401 agtcgcggcg gtggaggtta gacctcagtc ccagttgatg gcatggcccg ctgcgctcgc 3720  
403 tgttgcgggc tcagccccgg cctcatttgg agctccggcg ggggctgcac gctccggccg 3780  
405 attcctcgac agcgcgcgcg gcggcagccg caggagccgc ggtccgcggt ttggagcgac 3840  
407 cgcgcgtgag cccccatcc tcgtctggag cgtgctccag gaagcggcag gagtgggggt 3900  
409 gaggccgcct ccgaggcagg gatgcagcgg ctggcgcgcc gctagcgcac cgcagcacc 3960

Use of n and / or Xaa has been detected in the  
Sequence Listing. Review the Sequence Listing  
to ensure a corresponding explanation is present  
in the <220> to <223> fields of each sequence  
using n or Xaa

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/771,208

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Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

L:228 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:240 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:252 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:264 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:747 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:763 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:779 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:809 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:821 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:833 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:845 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:857 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:869 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:881 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:5087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:5395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:5439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:5469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:6659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:6661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:7101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
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L:10317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:11543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
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L:12533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:12739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:13435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:14005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:17465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:19205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:21047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:21055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20